

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/643,755

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) \_\_\_\_ contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) \_\_\_\_ missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) \_\_\_\_ missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 10 ☐ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence-Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) \_\_\_\_ are missing this mandatory field or its response.
- 12 ☒ Use of <220>Feature (NEW RULES) Sequence(s) <sup>#4</sup> are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING                      DATE: 08/30/2000  
 PATENT APPLICATION: US/09/643,755              TIME: 14:32:19

Input Set : A:\Sequence  
 Output Set: N:\CRF3\08302000\I643755.raw

Does Not Comply  
 Corrected Diskette Needed

4 <110> APPLICANT: van Rooijen, Gijs  
 5.        Keon, Richard Glenn  
 6        Boothe, Joseph  
 7        Shen, Yin  
 10 <120> TITLE OF INVENTION: Commercial Production of Chymosin in Plants  
 12 <130> FILE REFERENCE: 9369-153  
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/643,755  
 C--> 15 <141> CURRENT FILING DATE: 2000-08-23  
 17 <160> NUMBER OF SEQ ID NOS: 4  
 19 <170> SOFTWARE: PatentIn Ver. 2.0  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 1173  
 23 <212> TYPE: DNA  
 24 <213> ORGANISM: Bovine  
 26 <220> FEATURE:  
 27 <221> NAME/KEY: CDS  
 28 <222> LOCATION: (1)..(1173)  
 30 <400> SEQUENCE: 1  
 31 atg aac ttc ctt aag tct ttc cct ttc tac gct ttc ctt tgt ttc ggt    48  
 32 Met Asn Phe Leu Lys Ser Phe Pro Phe Tyr Ala Phe Leu Cys Phe Gly  
 33    1                      5                      10                      15  
 35 caa tac ttc gtt gct gtt act cac gct gct gag atc acc cgc att cct    96  
 36 Gln Tyr Phe Val Ala Val Thr His Ala Ala Glu Ile Thr Arg Ile Pro  
 37                      20                      25                      30  
 39 ctc tac aaa ggt aag tct ctc cgt aag gcg ctg aag gaa cat gga ctt    144  
 40 Leu Tyr Lys Gly Lys Ser Leu Arg Lys Ala Leu Lys Glu His Gly Leu  
 41                      35                      40                      45  
 43 cta gaa gac ttc ttg cag aaa caa cag tat ggc atc agc agc aag tac    192  
 44 Leu Glu Asp Phe Leu Gln Lys Gln Gln Tyr Gly Ile Ser Ser Lys Tyr  
 45                      50                      55                      60  
 47 tcc ggc ttc ggt gaa gtt gct agc gtg cca ctt acc aac tac ctt gat    240  
 48 Ser Gly Phe Gly Glu Val Ala Ser Val Pro Leu Thr Asn Tyr Leu Asp  
 49    65                      70                      75                      80  
 51 agt caa tac ttt ggg aag atc tac ctc gga acc ccg cct caa gag ttc    288  
 52 Ser Gln Tyr Phe Gly Lys Ile Tyr Leu Gly Thr Pro Pro Gln Glu Phe  
 53                      85                      90                      95  
 55 acc gtt ctc ttt gat act ggt tcc tct gac ttc tgg gtt ccc tct atc    336  
 56 Thr Val Leu Phe Asp Thr Gly Ser Ser Asp Phe Trp Val Pro Ser Ile  
 57                      100                      105                      110  
 59 tac tgc aag agc aat gcc tgc aag aac cac caa aga ttc gat ccg aga    384  
 60 Tyr Cys Lys Ser Asn Ala Cys Lys Asn His Gln Arg Phe Asp Pro Arg  
 61                      115                      120                      125  
 63 aag tgc tcc acc ttc cag aac tta ggc aaa ccc ttg tct ata cac tac    432  
 64 Lys Ser Ser Thr Phe Gln Asn Leu Gly Lys Pro Leu Ser Ile His Tyr  
 65                      130                      135                      140  
 67 ggt aca ggt agc atg caa gga atc tta ggc tat gat acc gtc act gtc    480  
 68 Gly Thr Gly Ser Met Gln Gly Ile Leu Gly Tyr Asp Thr Val Thr Val

see p. 4, 6

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Input Set : A:\Sequence  
 Output Set: N:\CRF3\08302000\I643755.raw

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69 145          150          155          160
71 tcc aac att gtg gac att caa cag aca gta gga ctt agc acc caa gaa 528
72 Ser Asn Ile Val Asp Ile Gln Gln Thr Val Gly Leu Ser Thr Gln Glu
73          165          170          175
75 cca ggt gat gtc ttc acc tat gca gaa ttc gat ggc atc ctt ggt atg 576
76 Pro Gly Asp Val Phe Thr Tyr Ala Glu Phe Asp Gly Ile Leu Gly Met
77          180          185          190
79 gca tac cca tcg ctc gcg tca gag tac tcg ata cct gtg ttt gac aac 624
80 Ala Tyr Pro Ser Leu Ala Ser Glu Tyr Ser Ile Pro Val Phe Asp Asn
81          195          200          205
83 atg atg aac cga cac cta gta gct caa gac ttg ttc tcg gtt tac atg 672
84 Met Met Asn Arg His Leu Val Ala Gln Asp Leu Phe Ser Val Tyr Met
85          210          215          220
87 gac agg aat ggc cag gag agc atg ctc acg ctt gga gct att gat cca 720
88 Asp Arg Asn Gly Gln Glu Ser Met Leu Thr Leu Gly Ala Ile Asp Pro
89 225          230          235          240
91 tcc tac tac aca gga tct ctt cac tgg gtt cca gtc act gtg cag cag 768
92 Ser Tyr Tyr Thr Gly Ser Leu His Trp Val Pro Val Thr Val Gln Gln
93          245          250          255
95 tac tgg caa ttc act gtg gac agt gtc acc atc agc ggt gtg gtt gtt 816
96 Tyr Trp Gln Phe Thr Val Asp Ser Val Thr Ile Ser Gly Val Val Val
97          260          265          270
99 gca tgt gaa ggt gga tgt caa gct atc ttg gat acc ggt acg tcc aag 864
100 Ala Cys Glu Gly Gly Cys Gln Ala Ile Leu Asp Thr Gly Thr Ser Lys
101          275          280          285
103 ctg gtc gga cct agc agc gac att ctc aac att cag caa gct att gga 912
104 Leu Val Gly Pro Ser Ser Asp Ile Leu Asn Ile Gln Gln Ala Ile Gly
105          290          295          300
107 gcc aca cag aac cag tac ggt gag ttt gac ata gat tgc gac aac ctt 960
108 Ala Thr Gln Asn Gln Tyr Gly Glu Phe Asp Ile Asp Cys Asp Asn Leu
109 305          310          315          320
111 agc tac atg cct aca gtt gtc ttt gag atc aac ggc aag atg tac cca 1008
112 Ser Tyr Met Pro Thr Val Val Phe Glu Ile Asn Gly Lys Met Tyr Pro
113          325          330          335
115 ctg acc ccc tcc gcc tat acc agc cag gat caa ggg ttc tgc acc agt 1056
116 Leu Thr Pro Ser Ala Tyr Thr Ser Gln Asp Gln Gly Phe Cys Thr Ser
117          340          345          350
119 gga ttc cag agt gag aac cat tcc cag aaa tgg atc ttg gga gat gtg 1104
120 Gly Phe Gln Ser Glu Asn His Ser Gln Lys Trp Ile Leu Gly Asp Val
121          355          360          365
123 ttc att cgt gag tac tac agc gtc ttt gac agg gcc aac aac ctc gtt 1152
124 Phe Ile Arg Glu Tyr Tyr Ser Val Phe Asp Arg Ala Asn Asn Leu Val
125          370          375          380
127 ggg cta gct aaa gca atc tga 1173
128 Gly Leu Ala Lys Ala Ile
129 385          390
132 <210> SEQ ID NO: 2
133 <211> LENGTH: 390
134 <212> TYPE: PRT

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## RAW SEQUENCE LISTING

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Input Set : A:\Sequence

Output Set: N:\CRF3\08302000\I643755.raw

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135 <213> ORGANISM: Bovine
137 <400> SEQUENCE: 2
138 Met Asn Phe Leu Lys Ser Phe Pro Phe Tyr Ala Phe Leu Cys Phe Gly
139 1 5 10 15
141 Gln Tyr Phe Val Ala Val Thr His Ala Ala Glu Ile Thr Arg Ile Pro
142 20 25 30
144 Leu Tyr Lys Gly Lys Ser Leu Arg Lys Ala Leu Lys Glu His Gly Leu
145 35 40 45
147 Leu Glu Asp Phe Leu Gln Lys Gln Gln Tyr Gly Ile Ser Ser Lys Tyr
148 50 55 60
150 Ser Gly Phe Gly Glu Val Ala Ser Val Pro Leu Thr Asn Tyr Leu Asp
151 65 70 75 80
153 Ser Gln Tyr Phe Gly Lys Ile Tyr Leu Gly Thr Pro Pro Gln Glu Phe
154 85 90 95
156 Thr Val Leu Phe Asp Thr Gly Ser Ser Asp Phe Trp Val Pro Ser Ile
157 100 105 110
159 Tyr Cys Lys Ser Asn Ala Cys Lys Asn His Gln Arg Phe Asp Pro Arg
160 115 120 125
162 Lys Ser Ser Thr Phe Gln Asn Leu Gly Lys Pro Leu Ser Ile His Tyr
163 130 135 140
165 Gly Thr Gly Ser Met Gln Gly Ile Leu Gly Tyr Asp Thr Val Thr Val
166 145 150 155 160
168 Ser Asn Ile Val Asp Ile Gln Gln Thr Val Gly Leu Ser Thr Gln Glu
169 165 170 175
171 Pro Gly Asp Val Phe Thr Tyr Ala Glu Phe Asp Gly Ile Leu Gly Met
172 180 185 190
174 Ala Tyr Pro Ser Leu Ala Ser Glu Tyr Ser Ile Pro Val Phe Asp Asn
175 195 200 205
177 Met Met Asn Arg His Leu Val Ala Gln Asp Leu Phe Ser Val Tyr Met
178 210 215 220
180 Asp Arg Asn Gly Gln Glu Ser Met Leu Thr Leu Gly Ala Ile Asp Pro
181 225 230 235 240
183 Ser Tyr Tyr Thr Gly Ser Leu His Trp Val Pro Val Thr Val Gln Gln
184 245 250 255
186 Tyr Trp Gln Phe Thr Val Asp Ser Val Thr Ile Ser Gly Val Val Val
187 260 265 270
189 Ala Cys Glu Gly Gly Cys Gln Ala Ile Leu Asp Thr Gly Thr Ser Lys
190 275 280 285
192 Leu Val Gly Pro Ser Ser Asp Ile Leu Asn Ile Gln Gln Ala Ile Gly
193 290 295 300
195 Ala Thr Gln Asn Gln Tyr Gly Glu Phe Asp Ile Asp Cys Asp Asn Leu
196 305 310 315 320
198 Ser Tyr Met Pro Thr Val Val Phe Glu Ile Asn Gly Lys Met Tyr Pro
199 325 330 335
201 Leu Thr Pro Ser Ala Tyr Thr Ser Gln Asp Gln Gly Phe Cys Thr Ser
202 340 345 350
204 Gly Phe Gln Ser Glu Asn His Ser Gln Lys Trp Ile Leu Gly Asp Val
205 355 360 365
207 Phe Ile Arg Glu Tyr Tyr Ser Val Phe Asp Arg Ala Asn Asn Leu Val

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Input Set : A:\Sequence  
Output Set: N:\CRF3\08302000\I643755.raw

```

208      370      375      380
210 Gly Leu Ala Lys Ala Ile
211 385      390
214 <210> SEQ ID NO: 3
215 <211> LENGTH: 3957
216 <212> TYPE: DNA
217 <213> ORGANISM: Artificial Sequence
219 <220> FEATURE:
220 <221> NAME/KEY: CDS
221 <222> LOCATION: (1554)..(2726)
223 <220> FEATURE:
224 <223> OTHER INFORMATION: Description of Artificial Sequence (Figure 2)
226 <400> SEQUENCE: 3
227 ctgcaggaat tcattgtact ccagtatca ttatagttaa agtttttggt ctctcgccgg 60
229 tggtttttta cctctattta aagggttttt ccacctaaaa attctgggtat cattctcact 120
231 ttacttggtta ctttaatttc tcataatctt tggttgaaat tatcacgctt ccgcacacga 180
233 tatccctaca aattttattat ttgttaaaca ttttcaaacc gcataaaaatt ttatgaagtc 240
235 ccgtctatct ttaatgtagt ctaacatttt catattgaaa tatataattt acttaatttt 300
237 agcgttggtta gaaagcataa agattttatt ttattcttct tcatataaat gtttaataata 360
239 caatataaac aaattcttta cottaagaag gatttcccat tttatatttt aaaaatataat 420
241 ttatcaaata tttttcaacc acgtaaatct cataataata agttgtttca aaagtaataa 480
243 aatttaactc cataattttt ttattcgact gatcttaaa caacacccag tgacacaact 540
245 agccattttt ttctttgaat aaaaaaatcc aattatcatt gtattttttt tatacaatga 600
247 aaatttcacc aaacaatcat ttgtggtatt tctgaagcaa gtcattgtat gcaaaattct 660
249 ataattccca ttgacacta cgggaagtaac tgaagatctg cttttacatg cgagacacat 720
251 cttctaaagt aattttaata atagttacta tattcaagat ttcataatc aaatactcaa 780
253 tattacttct aaaaaattaa ttagatataa ttaaaatatt acttttttaa ttttaagttt 840
255 aattgttgaa ttgtgacta ttgatttatt attctactat gtttaaattg ttttatagat 900
257 agtttaagt aaatataagt aatgtagtag agtgtagag tgttacccta aaccataaac 960
259 tataacattt atggtggact aattttcata tatttcttat tgcttttacc tttcttgggt 1020
261 atgtaagtcc gtaactagaa ttacagtggg ttgcatggc actctgtggt cttttgggtc 1080
263 atgcatgggt cttgcgcaag aaaaagacaa agaacaaaga aaaaagacaa aacagagaga 1140
265 caaaacgcaa tcacacaacc aactcaaatt agtcaactggc tgatcaagat cgccgcgtcc 1200
267 atgtatgtct aaatgccatg caaagcaaca cgtgcttaac atgcacttta aatggctcac 1260
269 ccactctaac ccacacacaa acacattgcc tttttcttca tcatcaccac aaccacctgt 1320
271 atatattcat tctcttcgcg cactcaatt tcttcacttc aacacacgtc aacctgcata 1380
273 tgcgtgtcat cccatgccca aatctccatg catgttccaa ccaccttctc tcttatataa 1440
275 tacctataaa tacctctaat atcactcact tctttcatca tccatccatc cagagtacta 1500
277 ctactctact actataatac cccaacccaa ctcatattca atactactct actatg 1556
278 Met
279 1
281 aac ttc ctt aag tct ttc cct ttc tac gct ttc ctt tgt ttc ggt caa 1604
282 Asn Phe Leu Lys Ser Phe Pro Phe Tyr Ala Phe Leu Cys Phe Gly Gln
283 5 10 15
285 tac ttc gtt gct gtt act cac gct gct gag atc acc cgc att cct ctc 1652
286 Tyr Phe Val Ala Val Thr His Ala Ala Glu Ile Thr Arg Ile Pro Leu
287 20 25 30
289 tac aaa ggt aag tct ctc cgt aag gcg ctg aag gaa cat gga ctt cta 1700
290 Tyr Lys Gly Lys Ser Leu Arg Lys Ala Leu Lys Glu His Gly Leu Leu

```

*More specific  
source of genetic  
material in the  
artificial sequence*

*See #12 on  
Error Summary  
Sheet.*

## RAW SEQUENCE LISTING

DATE: 08/30/2000

PATENT APPLICATION: US/09/643,755

TIME: 14:32:19

Input Set : A:\Sequence

Output Set: N:\CRF3\08302000\I643755.raw

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291      35      40      45
293 gaa gac ttc ttg cag aaa caa cag tat ggc atc agc agc aag tac tcc 1748
294 Glu Asp Phe Leu Gln Lys Gln Gln Tyr Gly Ile Ser Ser Lys Tyr Ser
295 50      55      60      65
297 ggc ttc ggt gaa gtt gct agc gtg cca ctt acc aac tac ctt gat agt 1796
298 Gly Phe Gly Glu Val Ala Ser Val Pro Leu Thr Asn Tyr Leu Asp Ser
299      70      75      80
301 caa tac ttt ggg aag atc tac ctc gga acc ccg cct caa gag ttc acc 1844
302 Gln Tyr Phe Gly Lys Ile Tyr Leu Gly Thr Pro Pro Gln Glu Phe Thr
303      85      90      95
305 gtt ctc ttt gat act ggt tcc tct gac ttc tgg gtt ccc tct atc tac 1892
306 Val Leu Phe Asp Thr Gly Ser Ser Asp Phe Trp Val Pro Ser Ile Tyr
307      100      105      110
309 tgc aag agc aat gcc tgc aag aac cac caa aga ttc gat ccg aga aag 1940
310 Cys Lys Ser Asn Ala Cys Lys Asn His Gln Arg Phe Asp Pro Arg Lys
311      115      120      125
313 tcg tcc acc ttc cag aac tta ggc aaa ccc ttg tct ata cac tac ggt 1988
314 Ser Ser Thr Phe Gln Asn Leu Gly Lys Pro Leu Ser Ile His Tyr Gly
315 130      135      140      145
317 aca ggt agc atg caa gga atc tta ggc tat gat acc gtc act gtc tcc 2036
318 Thr Gly Ser Met Gln Gly Ile Leu Gly Tyr Asp Thr Val Thr Val Ser
319      150      155      160
321 aac att gtg gac att caa cag aca gta gga ctt agc acc caa gaa cca 2084
322 Asn Ile Val Asp Ile Gln Gln Thr Val Gly Leu Ser Thr Gln Glu Pro
323      165      170      175
325 ggt gat gtc ttc acc tat gca gaa ttc gat ggc atc ctt ggt atg gca 2132
326 Gly Asp Val Phe Thr Tyr Ala Glu Phe Asp Gly Ile Leu Gly Met Ala
327      180      185      190
329 tac cca tcg ctc gcg tca gag tac tcg ata cct gtg ttt gac aac atg 2180
330 Tyr Pro Ser Leu Ala Ser Glu Tyr Ser Ile Pro Val Phe Asp Asn Met
331      195      200      205
333 atg aac cga cac cta gta gct caa gac ttg ttc tcg gtt tac atg gac 2228
334 Met Asn Arg His Leu Val Ala Gln Asp Leu Phe Ser Val Tyr Met Asp
335 210      215      220      225
337 agg aat ggc cag gag agc atg ctc acg ctt gga gct att gat cca tcc 2276
338 Arg Asn Gly Gln Glu Ser Met Leu Thr Leu Gly Ala Ile Asp Pro Ser
339      230      235      240
341 tac tac aca gga tct ctt cac tgg gtt cca gtc act gtg cag cag tac 2324
342 Tyr Tyr Thr Gly Ser Leu His Trp Val Pro Val Thr Val Gln Gln Tyr
343      245      250      255
345 tgg caa ttc act gtg gac agt gtc acc atc agc ggt gtg gtt gtt gca 2372
346 Trp Gln Phe Thr Val Asp Ser Val Thr Ile Ser Gly Val Val Val Ala
347      260      265      270
349 tgt gaa ggt gga tgt caa gct atc ttg gat acc ggt acg tcc aag ctg 2420
350 Cys Glu Gly Gly Cys Gln Ala Ile Leu Asp Thr Gly Thr Ser Lys Leu
351      275      280      285
353 gtc gga cct agc agc gac att ctc aac att cag caa gct att gga gcc 2468
354 Val Gly Pro Ser Ser Asp Ile Leu Asn Ile Gln Gln Ala Ile Gly Ala
355 290      295      300      305

```

09/64, 755

P. 6

Missing mandatory <220> and  
<223> features to explain  
artificial sequence. See # 12  
on Error Summary Sheet.

<210> 4

<211> 390

<212> PRT

<213> Artificial Sequence

<400> 4

Met Asn Phe Leu Lys Ser Phe Pro Phe Tyr Ala Phe Leu Cys Phe Gly

## VERIFICATION SUMMARY

DATE: 08/30/2000

PATENT APPLICATION: US/09/643,755

TIME: 14:32:20

Input Set : A:\Sequence

Output Set: N:\CRF3\08302000\I643755.raw

L:14 M:270 C: Current Application Number differs, Replaced Application Number  
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:429 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:429 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: